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Sim

Click [here](#) to view these alignments graphically with the [LALNVIEW](#) program (mime-type *chemical/x-aln2*).

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Results of SIM with:

Sequence 1: SEQ (434 residues)

Sequence 2: P10845, (1296 residues)

using the parameters:

Comparison matrix: BLOSUM62

Number of alignments computed: 5

Gap open penalty: 12

Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using [PRSS](#) at EMBnet-CH.

99.8% identity in 434 residues overlap; Score: 2296.0; Gap frequency: 0.0%

```
SEQ      1 MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
P10845,  863 LSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
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SEQ      61 KIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGE
P10845,  923 KIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGE
          *****

SEQ      121 IIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPIS
P10845,  983 IIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPIS
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SEQ      181 NLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWG
P10845,  1043 NLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGILKDFWG
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SEQ      241 DYLYQDKPYMYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFII
P10845,  1103 DYLYQDKPYMYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFII
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SEQ 301 KKYASGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
P10845, 1163 KKYASGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVV

SEQ 361 MKSKNDQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNQRQIERSSRTLGCWS
P10845, 1223 MKSKNDQGITNKCKMNLQDNNNGNDIGFIGFHQFNNAKLVASNWNQRQIERSSRTLGCWS

SEQ 421 EFIPVDDGWGERPL
P10845, 1283 EFIPVDDGWGERPE

34.8% identity in 23 residues overlap; Score: 41.0; Gap frequency: 0.0%

SEQ 207 IKYFNLFDKELNEKEIKDLYDNQ
P10845, 805 VKRLEDFDASLKDALLKYIYDNR
* * * * *

29.4% identity in 34 residues overlap; Score: 39.0; Gap frequency: 0.0%

SEQ 27 IDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
P10845, 367 LNFDAKAVFKINIVPKVNYTIYDGFNLRNTNLAAN
* * * * *



25.0% identity in 28 residues overlap; Score: 39.0; Gap frequency: 0.0%

SEQ 242 YLQYDKPYMYMLNLYDPNKYVDVNNVGIR
P10845, 366 YLNFDKAVFKINIVPKVNYTIYDGFNLR
* * * * *

31.8% identity in 22 residues overlap; Score: 37.0; Gap frequency: 0.0%

SEQ 344 LSALEIPDVGNLSQVVVMKSKN
P10845, 19 IAYIKIPNVGQMOPVKAFKIHN
* * * * *

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Search for

Range: from to
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 ☐ HPRD
 ☐ STS

☐ 1: P10845. Reports Botulinum neuroto...[gi:399133]
 [BLink](#), [Links](#)

LOCUS P10845 1296 aa linear BCT 01-MAY-2005
 DEFINITION Botulinum neurotoxin type A precursor (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain].
 ACCESSION P10845
 VERSION P10845 GI:399133
 DBSOURCE swissprot: locus BXA1_CLOBO, accession P10845; class: standard.
 extra accessions: P01561, P18639, created: Jul 1, 1989.
 sequence updated: Jul 1, 1993.
 annotation updated: May 1, 2005.
 xrefs: X52066.1, CAA36289.1, M30196.1, AAA23262.1, X92973.1, CAA63551.1, D67030.1, BAA11051.1, M27892.1, AAA23269.1, BTCLAB, 3BTAA
 xrefs (non-sequence databases): MEROPSM27.002, InterProIPR008985, InterProIPR011065, InterProIPR006025, InterProIPR000395, PfamPF01742, PRINTSPR00760, ProDomPD001963, PROSITEPS00142
 KEYWORDS 3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Pharmaceutical; Protease; Toxin; Transmembrane; Zinc.
 SOURCE Clostridium botulinum
 ORGANISM Clostridium botulinum
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
 REFERENCE 1 (residues 1 to 1296)
 AUTHORS Thompson, D.E., Brehm, J.K., Oultram, J.D., Swinfield, T.J., Shone, C.C., Atkinson, T., Melling, J. and Minton, N.P.
 TITLE The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding gene
 JOURNAL Eur. J. Biochem. 189 (1), 73-81 (1990)
 PUBMED 2185020
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=Type A / NCTC 2916
 REFERENCE 2 (residues 1 to 1296)
 AUTHORS Binz, T., Kurazono, H., Wille, M., Frevert, J., Wernars, K. and Niemann, H.
 TITLE The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins
 JOURNAL J. Biol. Chem. 265 (16), 9153-9158 (1990)
 PUBMED 2160960
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=Type A / 62A
 REFERENCE 3 (residues 1 to 1296)
 AUTHORS East, A.K., Bhandari, M., Stacey, J.M., Campbell, K.D. and Collins, M.D.
 TITLE Organization and phylogenetic interrelationships of genes encoding

components of the botulinum toxin complex in proteolytic Clostridium botulinum types A, B, and F: evidence of chimeric sequences in the gene encoding the nontoxic nonhemagglutinin component

JOURNAL Int. J. Syst. Bacteriol. 46 (4), 1105-1112 (1996)
PUBMED 8863443
REMARK NUCLEOTIDE SEQUENCE OF 1-65.
STRAIN=Type A / 62A

REFERENCE 4 (residues 1 to 1296)
AUTHORS Betley, M.J., Somers, E. and DasGupta, B.R.
TITLE Characterization of botulinum type A neurotoxin gene: delineation of the N-terminal encoding region

JOURNAL Biochem. Biophys. Res. Commun. 162 (3), 1388-1395 (1989)
PUBMED 2669749
REMARK NUCLEOTIDE SEQUENCE OF 1-34.
STRAIN=Type A / Hall

REFERENCE 5 (residues 1 to 1296)
AUTHORS Fujita, R., Fujinaga, Y., Inoue, K., Nakajima, H., Kumon, H. and Oguma, K.
TITLE Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins

JOURNAL FEBS Lett. 376 (1-2), 41-44 (1995)
PUBMED 8521962
REMARK NUCLEOTIDE SEQUENCE OF 1-18.
STRAIN=Type A / NIH

REFERENCE 6 (residues 1 to 1296)
AUTHORS Schmidt, J.J., Sathyamoorthy, V. and DasGupta, B.R.
TITLE Partial amino acid sequence of the heavy and light chains of botulinum neurotoxin type A

JOURNAL Biochem. Biophys. Res. Commun. 119 (3), 900-904 (1984)
PUBMED 6370252
REMARK PROTEIN SEQUENCE OF 1-16.

REFERENCE 7 (residues 1 to 1296)
AUTHORS Dasgupta, B.R., Foley, J. and Niece, R.
TITLE Partial sequence of the light chain of botulinum neurotoxin type A

JOURNAL Biochemistry 26, 4162-4162 (1987)
REMARK PROTEIN SEQUENCE OF 1-46.

REFERENCE 8 (residues 1 to 1296)
AUTHORS DasGupta, B.R. and Dekleva, M.L.
TITLE Botulinum neurotoxin type A: sequence of amino acids at the N-terminus and around the nicking site

JOURNAL Biochimie 72 (9), 661-664 (1990)
PUBMED 2126206
REMARK PROTEIN SEQUENCE OF 1-5 AND 444-456.

REFERENCE 9 (residues 1 to 1296)
AUTHORS Sathyamoorthy, V., Dasgupta, B.R., Foley, J. and Niece, R.L.
TITLE Botulinum neurotoxin type A: cleavage of the heavy chain into two halves and their partial sequences

JOURNAL Arch. Biochem. Biophys. 266 (1), 142-151 (1988)
PUBMED 3178218
REMARK PROTEIN SEQUENCE OF 448-464 AND 872-895.

REFERENCE 10 (residues 1 to 1296)
AUTHORS Shone, C.C., Hambleton, P. and Melling, J.
TITLE Inactivation of Clostridium botulinum type A neurotoxin by trypsin and purification of two tryptic fragments. Proteolytic action near the COOH-terminus of the heavy subunit destroys toxin-binding activity

JOURNAL Eur. J. Biochem. 151 (1), 75-82 (1985)
PUBMED 3896784

REMARK PROTEIN SEQUENCE OF 448-482.
REFERENCE 11 (residues 1 to 1296)
AUTHORS Gimenez, J.A. and DasGupta, B.R.
TITLE Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments
JOURNAL J. Protein Chem. 12 (3), 351-363 (1993)
PUBMED [8397793](#)
REMARK PROTEIN SEQUENCE OF 866-879 AND 1147-1218.
REFERENCE 12 (residues 1 to 1296)
AUTHORS Schiavo, G., Santucci, A., Dasgupta, B.R., Mehta, P.P., Jontes, J., Benfenati, F., Wilson, M.C. and Montecucco, C.
TITLE Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds
JOURNAL FEBS Lett. 335 (1), 99-103 (1993)
PUBMED [8243676](#)
REMARK IDENTIFICATION OF SUBSTRATE.
REFERENCE 13 (residues 1 to 1296)
AUTHORS Binz, T., Blasi, J., Yamasaki, S., Baumeister, A., Link, E., Sudhof, T.C., Jahn, R. and Niemann, H.
TITLE Proteolysis of SNAP-25 by types E and A botulinum neurotoxins
JOURNAL J. Biol. Chem. 269 (3), 1617-1620 (1994)
PUBMED [8294407](#)
REMARK IDENTIFICATION OF SUBSTRATE.
REFERENCE 14 (residues 1 to 1296)
AUTHORS Rigoni, M., Caccin, P., Johnson, E.A., Montecucco, C. and Rossetto, O.
TITLE Site-directed mutagenesis identifies active-site residues of the light chain of botulinum neurotoxin type A
JOURNAL Biochem. Biophys. Res. Commun. 288 (5), 1231-1237 (2001)
PUBMED [11700044](#)
REMARK MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
REFERENCE 15 (residues 1 to 1296)
AUTHORS Lacy, D.B., Tepp, W., Cohen, A.C., DasGupta, B.R. and Stevens, R.C.
TITLE Crystal structure of botulinum neurotoxin type A and implications for toxicity
JOURNAL Nat. Struct. Biol. 5 (10), 898-902 (1998)
PUBMED [9783750](#)
REMARK X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
COMMENT On or before Mar 15, 2005 this sequence version replaced [gi:279630](#), [gi:115193](#), [gi:115174](#).
[FUNCTION] Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-I-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure.
[CATALYTIC ACTIVITY] Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.
[COFACTOR] Binds 1 zinc ion per subunit.
[SUBUNIT] Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H).
[SUBCELLULAR LOCATION] Secreted.
[PHARMACEUTICAL] Available under the name BOTOX (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial

spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

[MISCELLANEOUS] There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.

[SIMILARITY] Belongs to the peptidase M27 family.

[DATABASE] NAME=BOTOX product information Web site;

WWW='<http://www.botox.com/site/>'.

[DATABASE] NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;

WWW='http://www.expasy.org/spotlight/back_issues/sptlt019.shtml'.

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gene	1..1296 /gene="botA" /note="synonyms: atx, bna"
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Region	2 /gene="botA" /region_name="Conflict" /note="P -> Q (in Ref. 1)." /evidence=experimental
Region	10..11 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
Region	19..23 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
Region	26 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
Region	27 /gene="botA" /region_name="Variant" /note="V -> A." /evidence=experimental
Region	33..39 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
Region	40..41 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
Region	42..48 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
Region	54..56

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Region 192..193
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Region 195..196
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Region 201..203
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Region 206..207
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Region 213..214
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Region 217..232
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Site 224

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Region 233..234

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Region 239..240
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Region 242
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Region      260..266
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Site 262

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Region 331..332
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Region 358..359
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Region 366..367
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Region 381..383
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Region 449..1296

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<u>Region</u>	/region_name="Helical region" /evidence=experimental 721 /gene="botA"
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<u>Region</u>	/region_name="Helical region" /evidence=experimental 825..829 /gene="botA"
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Region 860..871
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      /region_name="Helical region"
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Region 873..876
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      /region_name="Helical region"
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Region 876
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Region 885..886
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      /evidence=experimental
Region 887..890
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      /region_name="Beta-strand region"
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Region 891..892
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      /region_name="Hydrogen bonded turn"
      /evidence=experimental
Region 892
      /gene="botA"
      /region_name="Conflict"
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Region 905..906
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Region 911..912
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      /region_name="Hydrogen bonded turn"
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Region 913..917
      /gene="botA"
      /region_name="Beta-strand region"
      /evidence=experimental
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      /gene="botA"
      /region_name="Hydrogen bonded turn"
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Region 924..928
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      /region_name="Beta-strand region"
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<u>Region</u>	941..948 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	956..959 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	961..966 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	975..979 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	982..988 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	990..991 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	994..1000 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1011..1012 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1014..1021 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1023..1024 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
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<u>Region</u>	1032..1033 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1034..1040 /gene="botA" /region_name="Beta-strand region" /evidence=experimental

<u>Region</u>	1042..1043 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1052..1058 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1063..1064 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1066..1075 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1081..1090 /gene="botA" /region_name="Helical region" /evidence=experimental
<u>Region</u>	1091..1092 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
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<u>Region</u>	1100..1101 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1104 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1106 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1111..1113 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1119..1120 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
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<u>Region</u>	1134..1137 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1142 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1152 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1159..1163 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
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<u>Region</u>	1175 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1176..1177 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1179..1186 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1187..1188 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1189..1195 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1197..1198 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1207..1209 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1211..1213 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1215..1216 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental

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Region      1218
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               /region_name="Beta-strand region"
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Region      1228..1229
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               /region_name="Hydrogen bonded turn"
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Region      1232
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Bond        bond(1235,1280)
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               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1242..1243
               /gene="botA"
               /region_name="Hydrogen bonded turn"
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Region      1248..1253
               /gene="botA"
               /region_name="Beta-strand region"
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               /gene="botA"
               /region_name="Beta-strand region"
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Region      1265..1270
               /gene="botA"
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Region      1271..1272
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               /region_name="Hydrogen bonded turn"
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Region      1279..1280
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/region_name="Beta-strand region"
/evidence=experimental
Region 1284..1285
/gene="botA"
/region_name="Beta-strand region"
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Region 1289..1290
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ORIGIN

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121 stidtelkvi dtncinviqp dgsyrseeln lviigpsadi iqfecksfgh evlnltrngy
181 gstqyirfsp dftfgfeesl evdtnpllg gkfatdpavt laheliagh rlygiainp
241 rvfkvntnay yemsglevsf eelrtfgghd akfidslqen efrlyyyknf kdiastlnka
301 ksivgttasl qymknvfkek yllsedtsqk fsvdklkfdk lykmlteiyt ednfvkffkv
361 lnrktylnfd kavfkinivp kvnytiydgf nlrntnlaan fngqnteinn mnftklknft
421 glfeykllc vrgiitsktk sldkgynkal ndlcikvnnw dlffspsedn ftndlnkgee
481 itsdtnieaa eenisldliq qyyltfndfn epenisienl ssdiigglel mpnierfpng
541 kkyeldkytm fhylraqefe hgksrialtn svneallnps rvytffssdy vkkvnkatea
601 amflgwveql vydfdetse vstdtkiadi tiipyigpa lnignmlykd dfvgalifsg
661 avillefipe iaipvlgtfa lvsyiankv tvqtidnals krnekwdevy kyivtnwlak
721 vntqidlirk kmkealenqa eatkaiinyq ynqyteeeen ninfniddls sklmesinka
781 mininkflnq csvsylvmsm ipygvkrled fdaskdall kyidyndrgtl igqvdrldk
841 vnntlstdip fqlskyvdnq rllstfteyi kniintsiln lryesnhlid lsryaskini
901 gskvnfdpid knqiqlfnle sskievilk aivynsmyen fstsfwirip kyfnsislnd
961 eytiincmen nsgkwkslly geiiwtlqdt qeikqrvvfk ysqminisdy inrwifvtit
1021 nnrlnnskiy ingrlidqkp isnlgnihas nnimfkldgc rdthryiwik yfnlfdkeln
1081 ekeikdlydn qsnsgilkdf wgdylqydkp yymlnlydpn kyvdivnnvqi rgymylkgpr
1141 gsvmttniyl nsslyrgtkf iikkyasgnk dnivrnndrv yinvvvknke yrlatnasqa
1201 gvekilsale ipdvgnlsqv vvmkskndqg itnkckmnlq dnngndigfi gfhqfnniak
1261 lvasnwynrq ierssrtlgc swefipvddg wgerpl
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//

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[NCBI](#) | [NLM](#) | [NIH](#)

Feb 9 2005 14:31:10



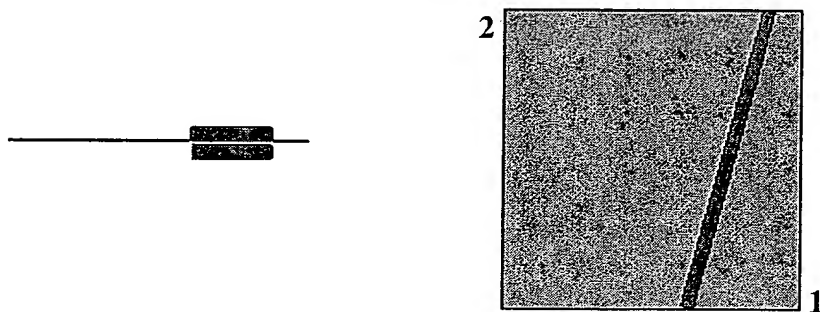
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2
x dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 1 [gi_144864](#) C.botulinum neurotoxin gene, complete cds. **Length** 4835 (1 .. 4835)

Length 1323 (1 .. 1323)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 412 bits (214), Expect = e-111
Identities = 937/1302 (71%)
Strand = Plus / Plus

Query: 2947 tctacatttactgaatatattaagaatattattaatacttctatattgaatttaagatat 3006
 ||||| || ||||| || ||||| || || ||||| || || ||||| | ||
 Sbjct: 16 tctaccttactgaatacatcaagaacatcatcaatacctccatcctgaacctgcgctac 75

```
Query: 3007 gaaagtaatcatttaatagacttatctaggtatgcatcaaaaataaatattggtagtaaa 3066
          |||  ||||  | || ||| | ||| | || || |||| || || ||| |||
Sbjct: 76   gaatccaatcacctgatcgacctgtctcgctacgcttcacaaatcaacatcggttctaaa 135
```

Query: 3067 gtaaattttgatccaatagataaaaaatcaaattcaattattttaatttagaaaagttagtaaa 3126
|| || | ||||| || || || ||||| || || | || || | ||| |
Sbjct: 136 gttaacttcgatccgatcgacaagaatcagatccagctgttcaatctggaatcttccaaa 195

Query: 3127 attgaggtaatTTTAAAAAatgctattgtatataatagtatgtatgaaaatttttagtact 3186
 || || || || | || ||||| |||| || ||||| ||||| || ||
 Sbjct: 196 atcgaagttatcctgaagaatgctatcgtatacaactctatgtacgaaaacttctccacc 255

Query: 3907 gtagtagttaaaaaataaagaatataggttagctactaatgcatcacaggcaggcgtagaa 3966
 || ||||| || ||||| | | |||| |||| || ||||| || |||||
 Sbjct: 976 gttgtagttaagaacaaagaataaccgtctggctaccaatgcttctcaggctgggtgtagaa 1035

Query: 3967 aaaataactaagtgcattagaaatacctgatgtaggaaatctaagtcaagtagtagtaatg 4026
 || || | ||| | |||| || || || |||| || || ||||| |||||
 Sbjct: 1036 aagatcttgtctgctctggaaatcccgacgttggaatctgtctcaggtagttgtaatg 1095

Query: 4027 aagtcaaaaaatgatcaaggaataacaaataaatgcaaaatgaatttacaagataataat 4086
 || || || || || || || || || || || ||||| ||||| || || || || ||
 Sbjct: 1096 aaatccaagaacgaccagggtatcactaacaatgcaaaatgaatctgcaggacaacaat 1155

Query: 4087 gggaaatgatataggctttataggatttcatcagtttaataatatagctaaactagtagca 4146
 || || |||| || || || || || || || || || || || || || || || || || ||
 Sbjct: 1156 ggtaacgatatcggtttcatcgggttccaccagttcaacaatatcgctaaactggttgct 1215

Query: 4147 agtaattggtataatagacaaatagaaagatctagtaggactttgggttgctcatgggaa 4206
 || |||| ||| | || || || || | || | || || ||||| |||||
 Sbjct: 1216 tccaactggtacaatcgtcagatcgaacgttcctctcgcactctgggttgctcttgggag 1275

Query: 4207 tttattcctgtagatgatggatggggagaaaggccactgtaa 4248
 || || || || || |||| || |||| || || || || || || || || || || || ||
 Sbjct: 1276 ttcacccggttgatgacggttggggtgaacgtccgctgtaa 1317

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped

Lambda	K	H
1.33	0.621	1.12

Matrix: blastn matrix:1 -2
 Gap Penalties: Existence: 5, Extension: 2
 Number of Sequences: 1
 Number of Hits to DB: 75
 Number of extensions: 6
 Number of successful extensions: 2
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's gapped: 1
 Number of HSP's successfully gapped: 1
 Number of extra gapped extensions for HSPs above 10.0: 0
 Length of query: 4835
 Length of database: 14,601,814,750
 Length adjustment: 27
 Effective length of query: 4808
 Effective length of database: 14,601,814,723
 Effective search space: 70205525188184
 Effective search space used: 70205525188184
 Neighboring words threshold: 0
 Window for multiple hits: 0
 X1: 11 (21.1 bits)

h cb hg b b e b cg

X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)

ALTNSVNEALLNPSRVYTFSSDYVKKVNKATEAMFLGWVEQLVYDFTDETSEVSTT
 DKIADITIIIPYIGPALNIGNMLYKDDFVGALIFSGAVILLEFIPEIAIPVLGTFALV
 SYIANKVLTQVIDNALSQRNEKWDEVYKYIVTNWLAKVNTQIDLIRKKMKEALENQA
 EATKAIINYQYNQYTEEEKNNINFNIDDLSSKLNESINKAMININKFLNQCSVSYLMN
 SMIPYGVKRLEDFDASLKDALLKYIYDNRGTLIGQVDRDKDKVNNTLSTDIPFQLSKY
 VDNQRLSTFTEYIKNIINTSILNLRYESNHLIDLRYASKINIGSKVNFDPIDKNQI
 QLFNLESSKIEVILKNAIVYNSMYENFSTFSWIRIPKYFNSISLNNEYTIINCMMENS
 GWKVSILNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIY
 INGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIWIKYFNLFDKELNEKEIKDLY
 DNQSNSSGILKDFWGDYLDQYDKPYMNLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTT
 NIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEK
 ILSALEIPDVGNLQVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNAKLK
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misc feature

4400..4432

/note="potential terminator; putative"

ORIGIN

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181 tatttatttc caattgttta accctatctt ataacggtaa atatatatgt ttatctatga
241 aagatgaaaa ccataattgg atgatatgta ataattgatat gtcaaagtat ttgtatttat
301 ggtcatttaa ataattaata atttaattaa ttttaaatat tataagaggt gttaaatatg
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481 atatgggtta ttccagaaaag agatacatat acaaatcctg aagaaggaga tttaaatcca
541 ccaccagaag caaaacaagt tccagtttca tattatgatt caacatatat aagtacagat
601 aatgaaaaag ataattatatt aaagggaggt acaaaattat ttgagagaat ttattcaact
661 gatcttggaa gaatgttggt aacatcaata gtaaggggaa taccattttg ggggtggaagt
721 acaatagata cagaattaaa agttattgat actaattgta ttaatgtgat acaaccagat
781 ggtagttata gatcagaaga acttaattcta gtaataatag gaccctcagc tgatattata
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1021 gcacatgaac ttatacatgc tggacataga ttatatggaa tagcaattaa tccaaatagg
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1861 tattatttaa cctttaattt tgataatgaa cctgaaaata tttcaataga aaatctttca
1921 agtgacatta taggccaatt agaacttatg cctaatatag aaagatttcc taatggaaaa
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2221 agtactacgg ataaaattgc ggatataact ataattattc catatatagg acctgcttta
2281 aatataggta atatgttata taaagatgat tttgtaggtg ctttaatat ttcaggagct
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2401 gtatcatata ttgcgaataa ggttctaacc gttcaaacia tagataatgc ttttaagtaa
2461 agaaatgaaa aatgggatga ggtctataaa tatatagtaa caaattgggt agcaaagggt
2521 aatacacaga ttgatctaata agaaaaaaa atgaaagaag ctttagaaaa tcaagcagaa
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2701 attaatataa ataaatTTTT gaatcaatgc tctgtttcat atttaatgaa ttctatgatc
2761 ccttatggtg tTaaacggtt agaagatttt gatgctagtc tTaaagatgc attattaaag
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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Range: from to ☐ Reverse complemented strand Features: ☐ SNP

☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [M30196](#). Reports *C.botulinum* neuro...[gi:144864] [Links](#)

LOCUS CLONEUR 4835 bp DNA linear BCT 26-APR-1993
DEFINITION *C.botulinum* neurotoxin gene, complete cds.
ACCESSION M30196
VERSION M30196.1 GI:144864
KEYWORDS neurotoxin.
SOURCE *Clostridium botulinum*
ORGANISM *Clostridium botulinum*
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium.
REFERENCE 1 (bases 1 to 4835)
AUTHORS Binz,T., Kurazono,H., Wille,M., Frevert,J., Wernars,K. and
Niemann,H.
TITLE The complete sequence of botulinum neurotoxin type A and comparison
with other clostridial neurotoxins
JOURNAL J. Biol. Chem. 265 (16), 9153-9158 (1990)
PUBMED 2160960
COMMENT Original source text: *C.botulinum* (strain 62A, subtype A) DNA.
Draft entry and computer-readable sequence for [1] kindly submitted
by H.Niemann, 29-NOV-1989.
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misc feature

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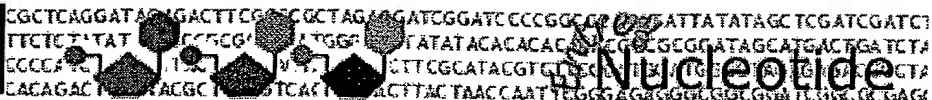
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☐ CDD ☒ MGC ☐ HPRD ☐ STS

☐ 1: [X52066](#). Reports *Clostridium botul...*[gi:40381]

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LOCUS CBBOTAG 4292 bp DNA linear BCT 12-SEP-1993
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 ACCESSION X52066 X52088
 VERSION X52066.1 GI:40381
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 ORGANISM *Clostridium botulinum*
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 Clostridium.
 REFERENCE 1 (bases 1 to 4292)
 AUTHORS Thompson,D.E., Brehm,J.K., Oultram,J.D., Swinfield,T.J.,
 Shone,C.C., Atkinson,T., Melling,J. and Minton,N.P.
 TITLE The complete amino acid sequence of the *Clostridium botulinum* type
 A neurotoxin, deduced by nucleotide sequence analysis of the
 encoding gene
 JOURNAL Eur. J. Biochem. 189 (1), 73-81 (1990)
 PUBMED 2185020
 REFERENCE 2 (bases 1 to 4292)
 AUTHORS Minton,N.P.
 TITLE Direct Submission
 JOURNAL Submitted (08-JAN-1990) Minton N.P., PHLS Centre for Applied
 Microbiology & Research, Molecular Genetics Group, Division of
 Biotechnology, Porton Down, Salisbury SP4 0JG Wiltshire, U K
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misc feature

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//

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Feb 9 2005 14:31:10

PubMed

Entrez

BLAST

OMIM

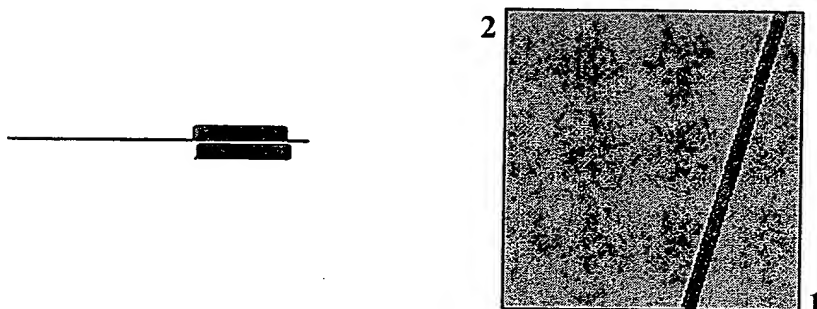
Taxonomy

Structure

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☒ Align

Sequence 2 lcl|seq 2

Length 1323 (1 .. 1323)

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 412 bits (214), Expect = e-111

Identities = 937/1302 (71%)

Strand = Plus / Plus

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Query: 2846 attgaggtaat~~ttt~~aaaaaatgctattgtatataatagtatgtatgaaaattttagtact 2905

Sbjct: 196 atcgaagttatcctgaagaatgctatcgatacaactctatgtacgaaaacttctccacc 255

[illegible]

h cb h g b b e b cg

X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 13 (25.7 bits)
S2: 22 (43.0 bits)



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Display Show

Range: from to Features:

1: [P04958](#). Reports Tetanus toxin pre...[gi:135624]

[BLink](#), [Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS P04958 1315 aa linear BCT 18-APR-2006
DEFINITION Tetanus toxin precursor (Tentoxylisin) [Contains: Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy chain (Tetanus toxin chain H)].
ACCESSION P04958
VERSION P04958 GI:135624
DBSOURCE swissprot: locus TETX_CLOTE, accession [P04958](#); class: standard. plasmid:pE88,7,created: Aug 13, 1987. sequence updated: Aug 13, 1987. annotation updated: Apr 18, 2006. xrefs: [X04436.1](#), [CAA28033.1](#), [X06214.1](#), [CAA29564.1](#), [AF528097.1](#), [AAO37454.1](#), [M12739.1](#), [AAA23282.1](#), [BTCLTN](#), [1A8D_](#), [1AF9_](#), [1D0HA](#), [1DFQA](#), [1DIWA](#), [1DLLA](#), [1FV2A](#), [1FV3A](#), [1FV3B](#), [1YVGA](#), [1YXWA](#), [1YYNA](#), [1Z7HA](#) xrefs (non-sequence databases): MEROPS:M27.001, GenomeReviews:AF528097_GR, LinkHub:P04958, InterPro:IPR011591, InterPro:IPR008985, InterPro:IPR013320, InterPro:IPR011065, InterPro:IPR006025, InterPro:IPR000395, InterPro:IPR013104, InterPro:IPR012928, InterPro:IPR012500, Pfam:PF01742, Pfam:PF07951, Pfam:PF07953, Pfam:PF07952, PRINTS:PR00760, ProDom:PD001963, PROSITE:PS00142
KEYWORDS 3D-structure; Complete proteome; Direct protein sequencing; Hydrolase; Metal-binding; Metalloprotease; Neurotoxin; Plasmid; Protease; Toxin; Zinc.
SOURCE Clostridium tetani
ORGANISM [Clostridium tetani](#) Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
REFERENCE 1 (residues 1 to 1315)
AUTHORS Eisel,U., Jarausch,W., Goretzki,K., Henschen,A., Engels,J., Weller,U., Hudel,M., Habermann,E. and Niemann,H.
TITLE Tetanus toxin: primary structure, expression in E. coli, and homology with botulinum toxins
JOURNAL EMBO J. 5 (10), 2495-2502 (1986)
PUBMED 3536478
REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA]. PLASMID=75 Kbp
REFERENCE 2 (residues 1 to 1315)
AUTHORS Fairweather,N.F. and Lyness,V.A.
TITLE The complete nucleotide sequence of tetanus toxin
JOURNAL Nucleic Acids Res. 14 (19), 7809-7812 (1986)
PUBMED 3774547

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN=CN3911; PLASMID=75 Kbp

REFERENCE 3 (residues 1 to 1315)
AUTHORS Brueggemann,H., Baeumer,S., Fricke,W.F., Wiezer,A., Liesegang,H.,
Decker,I., Herzberg,C., Martinez-Arias,R., Merkl,R., Henne,A. and
Gottschalk,G.
TITLE The genome sequence of Clostridium tetani, the causative agent of
tetanus disease
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (3), 1316-1321 (2003)
PUBMED [12552129](#)

REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=Massachusetts / E88; PLASMID=pE88

REFERENCE 4 (residues 1 to 1315)
AUTHORS Fairweather,N.F., Lyness,V.A., Pickard,D.J., Allen,G. and
Thomson,R.O.
TITLE Cloning, nucleotide sequencing, and expression of tetanus toxin
fragment C in Escherichia coli
JOURNAL J. Bacteriol. 165 (1), 21-27 (1986)
PUBMED [3510187](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 742-1314.
PLASMID=75 Kbp

REFERENCE 5 (residues 1 to 1315)
AUTHORS Krieglstein,K., Henschen,A., Weller,U. and Habermann,E.
TITLE Arrangement of disulfide bridges and positions of sulfhydryl groups
in tetanus toxin
JOURNAL Eur. J. Biochem. 188 (1), 39-45 (1990)
PUBMED [2108021](#)

REMARK PARTIAL PROTEIN SEQUENCE, AND DISULFIDE BONDS.

REFERENCE 6 (residues 1 to 1315)
AUTHORS Krieglstein,K.G., Henschen,A.H., Weller,U. and Habermann,E.
TITLE Limited proteolysis of tetanus toxin. Relation to activity and
identification of cleavage sites
JOURNAL Eur. J. Biochem. 202 (1), 41-51 (1991)
PUBMED [1935979](#)

REMARK PARTIAL PROTEIN SEQUENCE.

REFERENCE 7 (residues 1 to 1315)
AUTHORS Schiavo,G., Poulain,B., Rossetto,O., Benfenati,F., Tauc,L. and
Montecucco,C.
TITLE Tetanus toxin is a zinc protein and its inhibition of
neurotransmitter release and protease activity depend on zinc
JOURNAL EMBO J. 11 (10), 3577-3583 (1992)
PUBMED [1396558](#)

REMARK IDENTIFICATION AS ZINC-PROTEASE.

REFERENCE 8 (residues 1 to 1315)
AUTHORS Schiavo,G., Benfenati,F., Poulain,B., Rossetto,O., Polverino de
Laureto,P., DasGupta,B.R. and Montecucco,C.
TITLE Tetanus and botulinum-B neurotoxins block neurotransmitter release
by proteolytic cleavage of synaptobrevin
JOURNAL Nature 359 (6398), 832-835 (1992)
PUBMED [1331807](#)

REMARK IDENTIFICATION OF SUBSTRATE.

REFERENCE 9 (residues 1 to 1315)
AUTHORS Umland,T.C., Wingert,L.M., Swaminathan,S., Furey,W.F., Schmidt,J.J.
and Sax,M.
TITLE Structure of the receptor binding fragment HC of tetanus neurotoxin
JOURNAL Nat. Struct. Biol. 4 (10), 788-792 (1997)
PUBMED [9334741](#)

REMARK X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.

COMMENT On Apr 12, 2005 this sequence version replaced [gi:69647](#).
[FUNCTION] Tetanus toxin acts by inhibiting neurotransmitter

release. It binds to peripheral neuronal synapses, is internalized and moves by retrograde transport up the axon into the spinal cord where it can move between postsynaptic and presynaptic neurons. It inhibits neurotransmitter release by acting as a zinc endopeptidase that catalyzes the hydrolysis of the 76-Gln-|-Phe-77 bond of synaptobrevin-2.

[CATALYTIC ACTIVITY] Hydrolysis of 76-Gln-|-Phe-77 bond in synaptobrevin 2.

[COFACTOR] Binds 1 zinc ion per subunit (By similarity).

[SUBUNIT] The precursor polypeptide is subsequently cleaved to yield subchains L and H. These remain linked by a disulfide bridge and are non-toxic after separation.

[MISCELLANEOUS] The C-terminus of the heavy chain binds to ganglioside receptors.

[SIMILARITY] Belongs to the peptidase M27 family.

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<u>Site</u>	234 /gene="tetX" /locus_tag="CTC_p60" /site_type="active" /inference="non-experimental evidence, no additional details recorded" /note="By similarity."
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//

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Sim

Click here to view these alignments graphically with the LALNVIEW program (mime-type *chemical/x-aln2*).

Click here to download LALNVIEW (Unix, Mac and PC versions available).
You can also have a look at a sample screen of LALNVIEW and access its documentation.

Results of SIM with:

Sequence 1: SEQ (434 residues)
Sequence 2: TETX_CLOTE (1314 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 20
Gap open penalty: 12
Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using PRSS at EMBnet-CH.

33.9% identity in 434 residues overlap; Score: 496.0; Gap frequency:

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SEQ          14  TSILNLRYESNHLIDLSRYASKINIGSKVNFDP-IDKNQIQLFNLESSKIE
TETX_CLOTE   883  STILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESSEVI
                ****          * * *          * *      * * * * *

SEQ          73  NSMYENFSTSFWIRIPKYFNSISLN--NEytiINCMENNS-----GWKVS
TETX_CLOTE   943  NDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVS
                * *  **   *** * **   *          *** **  *   *      ** **

SEQ         125  LQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLID
TETX_CLOTE  1003  LKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDR LSSANLYINGVLMG
                * *          *          * * * * * * *      * * * *

SEQ         185  IHASNNIMFKLDGCRDTHRYIWIKYFNLFDKELNEKEIKDLYDNQSN SGIL
TETX_CLOTE  1063  IREDNNITLKLDR CNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLSITFLI

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          *   ***   ***   *           *   *   *   *   *   *   *   *   *
SEQ          245 YDKPYMYMLNLYDPNKYVDVNNVGIRGYMYL-KGPRGSVMTTNIYLNSSLYR(
TETX_CLOTE  1123 YDTEYYLIPVASSSKDVQLKN--ITDYMYLTNAPSYTNGKLNIIYRR-LYN(
          **   **           *   *   *   *   *   *   *   *   *   *

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SEQ          304 ASGNK-DNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIP-DV(
TETX_CLOTE  1180 TPNNEIDSFVKSGDFIKLYVSYNNEHIVGYPKDGNAFNNLDRILRVGYNAI
          *   *   *   *           *   *   *

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SEQ          362 KSKNDQGI-TNKCKMNLQDNNGNDIGFIGFH--QFNNTIAK---LVASNWYNI
TETX_CLOTE  1240 EAVKLRLDKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFI
          *           *   *           *   *   *   *   *   *   *   *

```

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SEQ          416 LGCSWEFIPVDDGW
TETX_CLOTE  1298 LGCDWYFVPTDEGW
          *** * * * * *

```

39.1% identity in 23 residues overlap; Score: 39.0; Gap frequency: 0

```

SEQ          141 QMINISDYINRWIFVTITNNRLN
TETX_CLOTE  1140 QLKNITDYMYLTNAPSYTNGKLN
          *   **   **           **   **

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31.4% identity in 35 residues overlap; Score: 35.0; Gap frequency: 0

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SEQ          81 TSFWIRIPKYFNSISLNNNEYTIINCMENNSGWKVS
TETX_CLOTE  213 TSLTIGKSKYFQDPALLMHელიHVLHGLYGMQVS
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```

32.6% identity in 46 residues overlap; Score: 33.0; Gap frequency: 2

```

SEQ          3 TFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPID
TETX_CLOTE  273 TFGGQDANLISIDIKNDLYEKT-LNDYKAIANKLSQVTSCNDPNID
          **           *   *   *   *   **   *   *   *   *   *

```

31.2% identity in 16 residues overlap; Score: 32.0; Gap frequency: 0

```

SEQ          155 VTITNNRLNNSKIYIN
TETX_CLOTE  1069 ITLKLDRCNNNNQYVS
          *           *   **   *

```

33.3% identity in 15 residues overlap; Score: 32.0; Gap frequency: 0

SEQ 96 LNNEYTIINCMENNS
TETX_CLOTE 117 LGNSYSLLDKFDTNS
* * * **

50.0% identity in 12 residues overlap; Score: 32.0; Gap frequency: 0

SEQ 162 LNNSKIYINGRL
TETX_CLOTE 1150 LTNAPSYTNGKL
* * * * *

36.8% identity in 19 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 3 TFTEYIKNIINTSILNLRY
TETX_CLOTE 204 TFDNVIENTISLTIGSKY
** * ** * *

27.8% identity in 18 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 245 YDKPYMMLNLYDPNKYVD
TETX_CLOTE 1169 YNGLKFIIKRYTPNNEID
* * ** *

50.0% identity in 12 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 62 IEVILKNAIVYN
TETX_CLOTE 876 IDVILKKSTILN
* **** *

40.0% identity in 15 residues overlap; Score: 31.0; Gap frequency: 0

SEQ 218 NEKEIKDLYDNQSNS
TETX_CLOTE 119 NSYSLLDKFDTNSNS
* * * ***

29.3% identity in 41 residues overlap; Score: 30.0; Gap frequency: 2

SEQ 35 KINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSM
TETX_CLOTE 542 KSNAASTIEIHNIDDNTIYQY-LYAQKSPTTLQRITMTNSV
* * * ** * * * **

21.7% identity in 23 residues overlap; Score: 30.0; Gap frequency: 0

SEQ 35 KINIGSKVNFDPIDKNQIQLFNL
TETX_CLOTE 365 KFNITRLSYFSMNHDPVKIPNL
* ** **

28.6% identity in 28 residues overlap; Score: 30.0; Gap frequency: 0

SEQ 316 DRVYINVVVKNKEYRLATNASQAGVEKI
TETX_CLOTE 278 DANLISIDIKNDLYEKTLDYKAIANKL
* * ** * * *

28.0% identity in 25 residues overlap; Score: 30.0; Gap frequency: 0

SEQ 142 MINISDYINRWIFVTITNNRLNNSK
TETX_CLOTE 789 MININIFMRESSRSFLVNQMINEAK
**** * * *

25.0% identity in 40 residues overlap; Score: 29.0; Gap frequency: 0

SEQ 211 NLFDKELNEKEIKDLYDNQSN SGILKDFWGDYLYQYDKPYY
TETX_CLOTE 617 DIIDDFTNES SQTTIDKISDVSTIVPYIGPALNIVKQGY
* ** * * * * *

22.8% identity in 79 residues overlap; Score: 29.0; Gap frequency: 3

SEQ 330 RLATNASQAGVEKILSALEIPDVG NLS-QVVMKSKNDQ-GITNKCKMNLQI
TETX_CLOTE 1225 RVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGI
* ** * * * * *

SEQ 388 IGFHQFN NIA-KLVASNWY
TETX_CLOTE 1285 ASNWYFNHLKDKILGCDWY
** * **

35.0% identity in 20 residues overlap; Score: 29.0; Gap frequency: 0

SEQ 362 KSKNDQGITNKCKMNLQDNN
TETX_CLOTE 333 KDSNGQYIVNEDKFQILYNS
* * * * *

42.9% identity in 14 residues overlap; Score: 28.0; Gap frequency: 0

SEQ 67 KNAIVYNSMYENFS
TETX_CLOTE 345 KFQILYNSIMYGFT
* * *** *

20.7% identity in 58 residues overlap; Score: 28.0; Gap frequency: 0

SEQ 307 NKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQ'
TETX_CLOTE 779 NKLEEKANKAMININIFMRESSRSFLVNQMINEAKKQLLEFDTQSKNILMQ'
* * * * *

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